

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1. (cancelled).

2 (currently amended). The method of Claim 4 55 wherein said collections are each defined as a vector representation of said plurality of function parameters.

3 (currently amended). The method of Claim 4 55 further comprising the steps of specifying at least a first threshold value delineating said plurality of functions of each of said collections.

4 (original). The method of Claim 3 wherein said at least a first threshold value is calculated based upon the likelihood of misclassification of data.

5 (original). The method of Claim 3 further comprising the step of segmenting the data according to said at least a first threshold value.

6 (previously presented). The method of Claim 3 wherein said collections are each defined as a vector representation of said plurality of function parameters.

7 (currently amended). The method of Claim 2 wherein said altering step is accomplished by evolving said plurality of collections according to a genetic, wherein said genetic algorithm includes a mutation operator comprising said randomly selecting, deleting, and adding steps.

8 (currently amended). The method of Claim 7 wherein said evolving includes crossover followed by said mutation operator.

9 (currently amended). The method of Claim 4 55 wherein said plurality of functions are normal distributions, and said plurality of functions parameters include the mean and standard deviations of said normal distributions.

10 (currently amended). The method of Claim 4 55 wherein said comparing step includes the utilization of a statistical f-test to evaluate the relative contribution of each of said plurality of functions in comparison of said fitting error and the data.

11 (currently amended). The method of Claim 4 55 wherein the data is organized as a histogram.

12 (currently amended). The method of Claim 4 55 wherein said stopping criteria are defined by a fitness function.

13 (previously presented). The method of Claim 12 wherein said fitness function is optimized to minimize the magnitude of the fit error between each of said collections and the data.

14 (currently amended). An apparatus for fitting a plurality of sub-population functions to digital image data, comprising:

means for defining a plurality of collections and a set of bins, each of said collections having a plurality an initial set of functions corresponding to different ones of said bins, said functions each having according to a plurality of function parameters and a total number of functions;

means for determining a fitting error between each a plurality of fitness values, each of said fitness values defining a difference between a respective one of said collections and the data;

means for comparing each said fitting error fitness value to stopping criteria to determine if said stopping criteria is satisfied;

means for altering said plurality of function parameters to provide a next generation of said collections and said total number of functions randomly in one or more of said collections, if said means for comparing determines that said fitting error stopping criteria is not satisfied; and

means for iterating said determining, comparing, and altering steps following said altering step;

wherein one or more of said iterated altering steps further comprise:

randomly selecting one of said collections of the respective said next generation and one of said bins;

if the randomly selected bin and one of said functions in the randomly selected collection correspond, deleting said corresponding function;

if the randomly selected bin has no corresponding function in the randomly selected collection, adding to the randomly selected collection a new function corresponding to said randomly selected bin, said new function having one or more randomly selected function parameters.

15 (previously presented). The apparatus of Claim 14 wherein said collections are each defined as a vector representation of said plurality of function parameters.

16 (original). The apparatus of Claim 14 further comprising means for specifying at least a first threshold value delineating said plurality of functions.

17 (original). The apparatus of Claim 16 wherein said at least a first threshold value is calculated based upon the likelihood of misclassification of data.

18 (original). The apparatus of Claim 16 further comprising means for segmenting the data according to said at least a first threshold value.

19 (cancelled).

20 (currently amended). The apparatus of Claim 15 wherein said means for altering operation is accomplished by evolving said plurality of

collections according to a genetic algorithm; wherein said genetic algorithm includes a mutation operator, said mutation operator comprising said randomly selecting, deleting, and adding steps.

21 (currently amended). The apparatus of Claim 20 wherein said genetic algorithm includes crossover followed by said mutation operator.

22 (original). The apparatus of Claim 14 wherein said plurality of functions are normal distributions, and said plurality of functions parameters include the mean and standard deviations of said normal distributions.

23 (original). The apparatus of Claim 14 wherein said means for comparing includes the utilization of a statistical f-test to evaluate the relative contribution of each of said plurality of functions in comparison of said fitting error and the data.

24 (original). The apparatus of Claim 14 wherein the data is organized as a histogram.

25 (original). The apparatus of Claim 14 wherein said stopping criteria are defined by a fitness function.

26 (previously presented). The apparatus of Claim 25 wherein said fitness function is optimized to minimize the magnitude of the fit error between said each of said collections and the data.

Claims 27-44 (cancelled).

45 (currently amended). A method of specifying thresholds for segmenting a digital image, comprising the steps of:

producing a histogram of the image, the histogram having histogram data, said histogram defining a plurality of bins;

defining a ~~collection~~ plurality of mixture models, each said mixture model being a combination of a plurality of subpopulations; wherein each

subpopulation is a function defined according to a plurality of function parameters;

defining a generation of chromosomes, each said chromosome being a vector ~~encoding a respective one of the mixture models wherein the elements of the vector encode the respective plurality of function parameters of the plurality of subpopulations having a plurality of elements, each said element corresponding to a respective one of said bins, each said element having a zero value or a non-zero value, each of said non-zero value elements encoding the function parameters of a respective one of said sub-populations;~~

for each chromosome in the generation, performing the following steps:

determining the fitting error between the mixture model defined by the chromosome and the histogram data;

determining a measure of the relative contributions of the individual sub-populations defined by the chromosome; and

determining a fitness value based on said fitting error and said measure of relative contributions;

comparing said fitness values to stopping criteria;

altering ~~said plurality of function parameters and said total number of functions in randomly selected~~ chromosomes of said generation to define a next generation of chromosomes, if none of said fitness values satisfies said stopping criteria; and

repeating said performing, comparing, and altering steps on said next generation of chromosomes, if none of said fitness values satisfies said stopping criteria, wherein one or more of said repeated altering steps further comprise:

randomly selecting one or more of said elements; and

replacing each of the randomly selected non-zero value

elements with a zero value element and each of the randomly selected zero value elements with a non-zero value element encoding randomly selected function parameters of a new sub-population; and

specifying at least a first threshold value delineating said sub-populations in a respective said mixture model, if at least one of said fitness values satisfies said stopping criteria.

46 (previously submitted). The method of Claim 45 wherein said at least a first threshold value is calculated based upon the likelihood of misclassification of said histogram data.

47-49 (cancelled).

50 (previously submitted). The method of Claim 45 wherein said plurality of functions are normal distributions, and said plurality of functions parameters include the mean and standard deviations of said normal distributions.

51 (previously submitted). The method of Claim 45 wherein said comparing step includes the utilization of a statistical f-test to evaluate the relative contribution of each of said plurality of functions in comparison of said fitting error and the data.

52 (previously submitted). The method of Claim 45 wherein said stopping criteria are defined by a fitness function.

53 (previously presented). The method of Claim 52 wherein said fitness function is optimized to minimize the magnitude of the fit error between said mixture model and the data.

54 (currently amended). An apparatus for specifying thresholds for segmenting a digital image, comprising ~~the steps of:~~

means for producing a histogram of the image, the histogram having histogram data, said histogram defining a plurality of bins;

means for defining a ~~collection~~ plurality of mixture models, each said mixture model being a combination of a plurality of subpopulations, wherein each subpopulation is a function defined according to a plurality of function parameters;

means for defining a generation of chromosomes, each said chromosome being a vector ~~encoding a respective one of the mixture models~~ ~~wherein the elements of the vector encode the respective plurality of function parameters of the plurality of subpopulations~~ having a plurality of elements, each

said element corresponding to a respective one of said bins, each said element having a zero value or a non-zero value, each of said non-zero value elements encoding the function parameters of a respective one of said sub-populations;

for each chromosome in the generation, means for performing the following steps:

determining the fitting error between the mixture model defined by the chromosome and the histogram data;

determining a measure of the relative contributions of the individual sub-populations defined by the chromosome; and

determining a fitness value based on said fitting error and said measure of relative contributions;

means for comparing said fitness values to stopping criteria;

means for altering said ~~plurality of function parameters and said total number of functions in randomly selected~~ chromosomes of said generation to define a next generation of chromosomes, if none of said fitness values satisfies said stopping criteria; and

means for repeating said performing, comparing, and altering steps on said next generation of chromosomes, if none of said fitness values satisfies said stopping criteria, wherein one or more of said repeated altering steps further comprise:

randomly selecting one or more of said elements; and  
replacing each of the randomly selected non-zero value  
elements with a zero value element and each of the randomly selected zero  
value elements with a non-zero value element encoding randomly selected  
function parameters of a new sub-population; and

means for specifying at least a first threshold value delineating said sub-populations in a respective said mixture model, if at least one of said fitness values satisfies said stopping criteria..

55 (new). A method of fitting a plurality of sub-population functions to digital image data, comprising the steps of:

defining a plurality of collections and a set of bins, each of said collections having an initial set of functions corresponding to different ones of said bins, said functions each having one or more function parameters;

determining a plurality of fitness values, each of said fitness values defining a difference between a respective one of said collections and the data;

comparing each said fitness value to stopping criteria to determine if said stopping criteria is satisfied;

if, at said comparing step, said stopping criteria is not satisfied, then altering said plurality of collections to provide a next generation of said collections; and

following said altering step, iterating said determining, comparing, and altering steps;

wherein one or more of said altering steps further comprise:

randomly selecting one of said collections of the respective said next generation and one of said bins;

if the randomly selected bin and one of said functions in the randomly selected collection correspond, deleting said corresponding function;

if the randomly selected bin has no corresponding function in the randomly selected collection, adding to the randomly selected collection a new function corresponding to said randomly selected bin, said new function having one or more randomly selected function parameters.

56 (new). The method of claim 55 wherein said altering further comprises randomly applying a genetic crossover operator to provide one or more pair of offspring collections, said deleting and adding being limited to said offspring collections.

57 (new). The method of claim 56 wherein said crossover operator is a single-point genetic crossover operator.